

Listing of Claims

1. (Canceled)

2. (Previously Presented) The method of claim 20, further comprising the steps of
(vi) preparing a separate heterologous gene construct for each isolated gene;
(vii) transforming plants with said separate heterologous gene construct wherein
expression of the isolated gene is enhanced in said plants; and
(viii) selecting plants having the desired trait.

3. (Currently Amended) The method of claim 20, wherein the enhancer element is
selected from the group consisting of a CaMV35S enhancer element, a Figwort Mosaic Virus (FMV)
promoter, a Figwort Mosaic Virus (FMV) enhancer, a peanut chlorotic streak caulimovirus full-length
transcript (PCISVFLt) sequence, and a mirabilis mosaic virus (MMV) promoter and a mirabilis mosaic
virus (MMV) enhancer.

4. (Currently Amended) The method of claim 3, wherein said enhancer element is the
CaMV35S enhancer element, and wherein the CaMV35S enhancer element is a 4X tandem duplicated
CaMV35S enhancer element having the sequence presented as SEQ ID NO:1.

5. (Currently Amended) The method of claim 3, wherein said enhancer element is the
Figwort Mosaic Virus (FMV) promoter having the sequence presented as SEQ ID NO:5 or the Figwort
Mosaic Virus (FMV) enhancer having the sequence presented as SEQ ID NO:6.

6. (Currently Amended) The method of claim 3, wherein said enhancer element is the
peanut chlorotic streak caulimovirus full-length transcript (PCISVFLt) sequence, and wherein the
PCISVFLt sequence is the enhancer having the sequence presented as SEQ ID NO:7.

7. (Currently Amended) The method of claim 3, wherein said enhancer element is the
mirabilis mosaic virus (MMV) promoter having the sequence presented as SEQ ID NO:8 or the
mirabilis mosaic virus (MMV) enhancer having the sequence presented as nucleotides 1-260 of SEQ
ID NO:8.

8. (Previously Presented) The method of claim 20, wherein said selectable marker-encoding nucleotide sequence encodes a polypeptide which confers herbicide-resistance to transformed plant cells expressing said marker.

9. (Previously Presented) The method of claim 20, wherein said selectable marker-encoding nucleotide sequence encodes an antibiotic resistance gene which confers resistance to an antibiotic selected from the group consisting of kanamycin, G418, bleomycin, hygromycin, chloramphenicol, ampicillin and tetracycline.

10. (Previously Presented) The method of claim 9, wherein said antibiotic is kanamycin.

11-15. (Canceled)

16. (Previously Presented) The method of claim 20, wherein said desired trait is a biochemical modification of a plant and fruit selected from the group consisting of a change in the level of vitamins, minerals, elements, amino acids, carbohydrates, lipids, nitrogenous bases, isoprenoids, phenylpropanoids and alkaloids.

17. (Previously Presented) The method of claim 20, wherein said desired trait is a fruit-bearing plant specific trait selected from the group consisting of increased resistance to fungal pathogens, increased resistance to bacterial pathogens, increased resistance to viral pathogens, increased resistance to insects, modified flower size, modified flower number, modified flower pigmentation, modified flower shape, modified leaf number, modified leaf pigmentation, modified flower shape, modified seed number, a modified pattern of leaves and flowers, a modified distribution of leaves and flowers, modified stem length between nodes, modified root mass, increased drought tolerance, increased salt tolerance and increased antibiotic tolerance.

18. (Canceled)

19. (Previously Presented) The method of claim 2, wherein the expression of the isolated gene is associated with a morphological characteristic selected from the group consisting of leaflet

size, leaf size, leaf color, leaf shape, leaflet number, leaf number, internode length, plant height, floral organ characteristics and fruit characteristics.

20. (Currently Amended) A method for identifying genes associated with a desired trait in a tomato plant comprising:

- (i) transforming cells of a tomato plant with a plant cell expression vector having an *E. coli* origin of replication, an enhancer element, a selectable marker-encoding nucleotide sequence operably linked to a promoter effective to express the selectable marker encoding sequence, a transcription termination element for said selectable marker-encoding nucleotide sequence and a T-DNA sequence in a manner effective to express said selectable marker-encoding nucleotide sequence;
- (ii) selecting plant cells which have been transformed by their ability to grow in the presence of an amount of selective agent that is toxic to non-transformed plant cells;
- (iii) regenerating transformed plant cells to yield mature plants;
- (iv) selecting plants having a desired trait; and
- (v) identifying, isolating and characterizing genes the transcription of which was enhanced by said enhancer element.

21. (Currently Amended) The method of claim 20 wherein said transforming cells is by infecting the cells with *Agrobacterium tumefaciens* tumefaciens in the absence of feeder cells, wherein said cells are hypocotyl cells from said tomato plant.

22. (Currently Amended) The method of claim 20 wherein said transforming cells is by infecting the cells with *Agrobacterium tumefaciens* tumefaciens in the absence of feeder cells, wherein said cells are shoot tip cells from said tomato plant.

23. (Previously Presented) The method of claim 20 wherein said tomato plant is a dwarf tomato plant.

24. (New) A method for identifying genes associated with a desired trait in a tomato plant comprising:

- (i) transforming cells of a tomato plant with a plant cell expression vector having an *E. coli* origin of replication, an enhancer element, a selectable marker-encoding nucleotide

sequence operably linked to a promoter effective to express the selectable marker encoding sequence, a transcription termination element for said selectable marker-encoding nucleotide sequence and a T-DNA sequence in a manner effective to express said selectable marker-encoding nucleotide sequence;

(ii) selecting plant cells which have been transformed by their ability to grow in the presence of an amount of selective agent that is toxic to non-transformed plant cells;

(iii) regenerating transformed plant cells to yield mature plants;

(iv) selecting plants having a desired trait, which selected plants are a subset of the regenerated plants, and which desired trait is different from the ability to grow in the presence of the selective agent that is toxic to non-transformed plant cells; and

(v) identifying, isolating and characterizing genes the transcription of which was enhanced by said enhancer element.